2002:90560 CAPLUS
DOCUMENT NUMBER: 136:146111
TITLE: Method for determining mRNA tissue distribution using restriction endonuclease digestion and PCR amplification for database indexing and drug screening
INVENTOR(S): Hilbush, Brian S.; Hasel, Karl W.; Sutcliffe, J. Gregor; Chang, Hwai Wen; Callahan, Marie Lei A.; Quan, Jeanette
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 41 pp., Cont.-in-part of U.S. Ser. No. 186,869.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002012922	A1	20020131	US 2001-775217	20010201
WO 2000026406	A1	20000511	WO 1999-US23655	19991014
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2002061045	A2	20020808	WO 2002-US2666	20020201
WO 2002061045	A3	20040212		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002243720	A1	20020812	AU 2002-243720	20020201

PRIORITY APPLN. INFO.:		
US 1998-186869	A2	19981104
WO 1999-US23655	W	19991014
US 2001-775217	A	20010201
WO 2002-US2666	W	20020201

AB An simplified method for the simultaneous sequence-specific identification of mRNAs in a mRNA population allowing the visualization of nearly every mRNA expressed by a tissue as a distinct band on a gel whose intensity corresponds roughly to the concentration of the mRNA without the need to prepare libraries is described. In general, the method comprises the formation of cDNA using anchor primers to fix a 3'-endpoint, ligating the cDNA to an adaptor containing a bacteriophage-specific promoter for subsequent RNA synthesis, generating linearized fragments of the cloned inserts by restriction endonuclease digestion, preparing cRNA, transcribing cDNA from the cRNA, and performing two sequence-specific PCR amplifications of the cDNA. The products of the second PCR amplification step are resolved by gel electrophoresis to obtain the length and the amount of each. In preferred embodiments, the method comprises comparing the length and at least part of the nucleotide sequence of the PCR products to expected values determined from a database of nucleotide sequences. Such database containing information on mRNA sequences, gene mapping, and cellular

distribution is further claimed. The method can identify changes in expression of mRNA associated with the administration of drugs or with physiol. or pathol. conditions. Also provided are vectors, host cells, and primers useful for the practice of the improved method. The primers are preferably labeled and contain phosphorothioate linkages. Two mRNA samples from serum-starved and serum-added human MG63 osteosarcoma cells were analyzed by the method of this invention with results showing significant improvement over the previous method using only one PCR step.

L7 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2000:314865 CAPLUS
DOCUMENT NUMBER: 132:344077
TITLE: Method for determining mRNA tissue distribution using restriction endonuclease digestion and PCR amplification for database indexing and drug screening
INVENTOR(S): Hasel, Karl W.; Hilbush, Brian S.
PATENT ASSIGNEE(S): Digital Gene Technologies, Inc., USA
SOURCE: PCT Int. Appl., 114 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000026406	A1	20000511	WO 1999-US23655	19991014
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2350168	AA	20000511	CA 1999-2350168	19991014
EP 1127159	A1	20010829	EP 1999-954838	19991014
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2002528135	T2	20020903	JP 2000-579778	19991014
US 2002012922	A1	20020131	US 2001-775217	20010201
NO 2001002203	A	20010702	NO 2001-2203	20010503
PRIORITY APPLN. INFO.:			US 1998-186869 A	19981104
			WO 1999-US23655 W	19991014

AB An improved method for the simultaneous sequence-specific identification of mRNAs in a mRNA population allows the visualization of nearly every mRNA expressed by a tissue as a distinct band on a gel whose intensity corresponds roughly to the concentration of the mRNA. In general, the method comprises the formation of cDNA using anchor primers to fix a 3'-endpoint, producing cloned inserts from the cDNA in a vector containing a bacteriophage-specific promoter for subsequent RNA synthesis, generating linearized fragments of the cloned inserts by restriction endonuclease digestion, preparing cRNA, transcribing cDNA from the cRNA , and performing two sequence-specific PCR amplifications of the cDNA. The products of the second PCR amplification step are resolved by gel electrophoresis to obtain the length and the amount of each. In preferred embodiments, the method comprises comparing the length and at least part of the nucleotide sequence of the PCR products to expected values determined from a database of nucleotide sequences. Such database containing information on mRNA sequences, gene mapping, and cellular distribution is further claimed. The method can identify changes in expression of mRNA associated with the administration of drugs or with physiol. or pathol. conditions.

Also provided are vectors, host cells, and primers useful for the practice of the improved method. The primers are preferably labeled and contain phosphorothioate linkages. Two mRNA samples from serum-starved and serum-added human MG63 osteosarcoma cells were analyzed by the method of this invention with results showing significant improvement over the previous method using only one PCR step.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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     (FILE 'HOME' ENTERED AT 16:29:09 ON 17 JUL 2006)

     FILE 'MEDLINE, CAPLUS, EMBASE, BIOTECHDS, BIOSIS, SCISEARCH' ENTERED AT
     16:29:57 ON 17 JUL 2006
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L2            33 S L1 AND PHOSPHOROTHIOATE
L3             1 S L2 AND (MICROARRAY OR BIOCHIP OR ARRAY OR BIOARRAY)
L4             3 S L2 AND (IN VITRO TRANSCRIPTION)
L5             3 DUP REM L4 (0 DUPLICATES REMOVED)
L6             6 S L2 AND TRANSCRIPTION
L7             6 DUP REM L6 (0 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 16:49:18 ON 17 JUL 2006

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